

SCORE Search Results Details for Application 10552515 and Search Result 20080624_135838_us-10-552-515-1_copy_157_933.ra1.

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Page	List	Overview	FAQ	Suggestions.

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135838_us-10-552-515-1_copy_157_933.ra1.

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OM protein - protein search, using sw model

Run on: June 24, 2008, 15:22:38 ; Search time 279 Seconds
(without alignments)
518.704 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNNTTVHYALLSASW.....SELSSHWTPTVTPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1143754 seqs, 186252778 residues

Total number of hits satisfying chosen parameters: 1143754

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /ABSS/Data/CRF/ptodata/1/iaa/5_COMB.pep:*
2: /ABSS/Data/CRF/ptodata/1/iaa/6_COMB.pep:*
3: /ABSS/Data/CRF/ptodata/1/iaa/7_COMB.pep:*
4: /ABSS/Data/CRF/ptodata/1/iaa/H_COMB.pep:*
5: /ABSS/Data/CRF/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /ABSS/Data/CRF/ptodata/1/iaa/RE_COMB.pep:*
7: /ABSS/Data/CRF/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		% Match	Length			
1	1502.5	36.4	920	2	US-10-104-047-2574	Sequence 2574, Ap
2	1154	28.0	596	2	US-10-104-047-2541	Sequence 2541, Ap
3	912.5	22.1	475	2	US-10-104-047-3116	Sequence 3116, Ap
4	873.5	21.2	642	3	US-10-108-260A-4483	Sequence 4483, Ap
5	796	19.3	425	2	US-09-270-767-45552	Sequence 45552, A
6	684.5	16.6	483	3	US-10-108-260A-3990	Sequence 3990, Ap
7	594.5	14.4	660	3	US-10-108-260A-3644	Sequence 3644, Ap
8	411.5	10.0	393	3	US-09-876-997-457	Sequence 457, App
9	411.5	10.0	393	3	US-10-643-836-457	Sequence 457, App
10	396.5	9.6	215	2	US-09-270-767-61064	Sequence 61064, A
11	329.5	8.0	366	2	US-09-270-767-32253	Sequence 32253, A
12	329.5	8.0	366	2	US-09-270-767-47470	Sequence 47470, A
13	290	7.0	189	2	US-09-270-767-31816	Sequence 31816, A
14	290	7.0	189	2	US-09-270-767-47033	Sequence 47033, A
15	255.5	6.2	199	2	US-09-270-767-31722	Sequence 31722, A
16	255.5	6.2	199	2	US-09-270-767-46939	Sequence 46939, A
17	186.5	4.5	166	2	US-09-621-976-4064	Sequence 4064, Ap
18	113.5	2.8	631	3	US-10-369-493-12179	Sequence 12179, A
19	108.5	2.6	523	2	US-09-949-016-11540	Sequence 11540, A
20	107.5	2.6	1107	3	US-11-216-782-11586	Sequence 11586, A
21	106.5	2.6	2013	1	US-08-324-977-12	Sequence 12, Appl
22	106.5	2.6	2013	1	US-08-384-616-12	Sequence 12, Appl
23	106.5	2.6	2013	1	US-08-904-686A-12	Sequence 12, Appl
24	106.5	2.6	2013	2	US-09-315-850-12	Sequence 12, Appl
25	106.5	2.6	3010	1	US-08-324-977-2	Sequence 2, Appli
26	106.5	2.6	3010	1	US-08-324-977-14	Sequence 14, Appl
27	106.5	2.6	3010	1	US-08-384-616-2	Sequence 2, Appli
28	106.5	2.6	3010	1	US-08-384-616-14	Sequence 14, Appl
29	106.5	2.6	3010	1	US-08-904-686A-2	Sequence 2, Appli
30	106.5	2.6	3010	1	US-08-904-686A-14	Sequence 14, Appl
31	106.5	2.6	3010	2	US-09-315-850-2	Sequence 2, Appli
32	106.5	2.6	3010	2	US-09-315-850-14	Sequence 14, Appl
33	106	2.6	539	2	US-09-248-796A-16542	Sequence 16542, A
34	105	2.5	1089	2	US-10-012-231A-102	Sequence 102, App
35	105	2.5	1089	2	US-10-015-389A-102	Sequence 102, App
36	105	2.5	1089	2	US-10-006-768A-102	Sequence 102, App
37	105	2.5	1089	2	US-10-015-671A-102	Sequence 102, App
38	105	2.5	1089	2	US-10-015-393A-102	Sequence 102, App
39	105	2.5	1089	2	US-10-011-833A-102	Sequence 102, App
40	105	2.5	1089	2	US-10-006-041A-102	Sequence 102, App
41	105	2.5	1089	2	US-10-012-064A-102	Sequence 102, App
42	105	2.5	1089	2	US-10-015-392A-102	Sequence 102, App
43	105	2.5	1089	3	US-10-011-795B-102	Sequence 102, App
44	105	2.5	1089	3	US-10-015-386A-102	Sequence 102, App
45	105	2.5	1089	3	US-10-012-121A-102	Sequence 102, App

ALIGNMENTS

RESULT 1

US-10-104-047-2574
 ; Sequence 2574, Application US/10104047
 ; Patent No. 6943241
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. 6943241el full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2574
 ; LENGTH: 920
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-2574

Query Match 36.4%; Score 1502.5; DB 2; Length 920;
 Best Local Similarity 40.4%; Pred. No. 2e-150;
 Matches 328; Conservative 145; Mismatches 270; Indels 69; Gaps 20;

Qy	8	NTTVHYALLSASWAVLCYYAEDLRCLKPLQE----	LPNQASNWS-----	AGLLAWLGIP	57
		: : : : : : : :			
Db	122	NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFM	SRIDKQISRLRRWLPKK	181	
Qy	58	NVLL--EVVPDVP--EYYSRFRVKNLPRFLGSDNQDTFTTSTKR	HQILFEILAKTPYGH	114	
		: : : : : : : : : : :			
Db	182	PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA	TRSRIVVHHILQRIKY-E	239	
Qy	115	EKKNLLGIHQLLAEGVLSAAFLPHDGFKTPPEGPQAPRLNQR	QVLFQHWARWGKWNKYQ	174	
		: : : : : : :			
Db	240	BGKNKIGLNRLLTNGSYEAAFLHEGSYRSKNSIRTHGAENHR	HLLYECWASWGVVYKYQ	299	
Qy	175	PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGC	FLVFSDIPTQELCGSKDS	234	
		: : : : : :			
Db	300	PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFGLFVFLYGV	TTLDHSQVSKEVCQATDI	359	
Qy	235	FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM	ALWAVLLLEYWKRKSATLA	293	
		: : : : : : : :			
Db	360	I-MCPVCCKYCFPMRLSDSCVYAKVTHLFDNGATVFVAFV	MAVWATVFLFVWKRRAVIA	418	
Qy	294	YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFP	ERSRARRMLAGSVVIVMV	352	
		: : : : : : : : :			
Db	419	YDWDLDIWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQA	FTDKCSRLIVSASGIFEMI	478	
Qy	353	AVVVMCLVSIIILYRAIMAIIVSRSGNTLLA-AWA-----	SRIASLTGSVV--NLVFILIL	404	
		: : : : : : : : : : :			

Db		479	CVVIAAVFGIVIRYRVTV-----STFAAFKVALIRNNSQVAT-TGTAVCINFCIIMLL	530
Qy		405	SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFISSPVYIAFFKGRFVGYPGNY	464
			: : : : : : :: : : :	
Db		531	NVLYEKVALLLTNLEQPRTSEWENSFTLKMFLQFVNLNSSTFYIAFFLRGRTGHPGAY	590
Qy		465	HTLFG-VRNEECAAGGLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQFRLRSKKR	523
			: ::: : :: : ::	
Db		591	LRLINRWRLIEECHPSGLCIDLCMQMGIIMVLKQTWNFMELGYPLIQNWWT--RRKVQR	647
Qy		524	KAGASAGASQGWPWEDDYELVPCE--GLDFEYLEMVLFQGFVTIFVAACPLAPLALLNNW	581
			: :	
Db		648	EHGPERKISFPQWEKDYNLQPMNAYGLDFEYLEMILQFGFTTIFVAAFPLAPLLALLNNI	707
Qy		582	VEIRLDARKFVCEYRRPVAERAQDIGIWPHILAGLTHLAVISNAFLAFSSDFLPRAYYR	641
			: : : : : : : : : : : : :	
Db		708	IEIRLDAYKFVTQWRRLASRAKDIGIWIYGILEGIGILSVITNAFVIAITSDFIPRLVYA	767
Qy		642	W-----TRAHDLRGLGNFTLA-----RAPSSFAAAHNRTCRYRAFR	677
			: : : : : : : : : : :	
Db		768	YKYGPCAQQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGEFSGTPLKYCRYRDYR	827
Qy		678	DDDGH----YSQTYWNLLAIRLAFVIHFHVVSVGRLLDLLVPDIPESVEIKVKREYY	732
			: : : : : : : : : : :	
Db		828	DPPHSLVPGYTQLQFWHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLDRDMRREKY	887
Qy		733	LAKQALAENEVLFGTNGTKDEQPKGSELSSHW	764
			: : : : : : :	
Db		888	LIOEMMYEAELERLOKERKCKKNGKAHHNEW	919

RESULT 2

```

US-10-104-047-2541
; Sequence 2541, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2541
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2541

```

Query Match 28.0%; Score 1154; DB 2; Length 596;
Best Local Similarity 41.3%; Pred. No. 1.7e-113;

	Matches	250;	Conservative	108;	Mismatches	194;	Indels	54;	Gaps	14;
Qy	201	LLPAAVVGTVLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAG	259							
Db	2	LFPAAFIGLVFLVLYGVTTLDSQVSKVCQATDII-MCPVCCKYCPMRLSDSCVYAKVT	60							
Qy	260	RLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APM	318							
Db	61	HLFDNGATVFFAVFMAVWATVLEFWKRRRAVIAYDWDLDWEEEEEEIRPQFEAKYSKK	120							
Qy	319	TAPNPITGEDEPYFPERSRARMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGN	378							
Db	121	ERMNPISGKPEPYQAFDTKCSRILVSASGIFFMICVVIAAVFGIVIVRVVTV-----S	173							
Qy	379	TLLA-AWA-----SRIASLTGSVV--NLVFIILSKIYVSLAHVLRWEMHRTQTKFEDA	430							
Db	174	TFAAFKQWALIRNNSQVAT-TGTAVCFNFCIIMLLNVLYEKVALLLTNLEQPRTESEWENS	232							
Qy	431	FTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELL	489							
Db	233	FTLKMFLQFVNLSSTFYIAFFLGRFTGHPGAYLRRLINRWLEECHPSGCLIDLQCMQMG	292							
Qy	490	VIMVGKQVINNMQEVLIPLKLGWWQKFLRLSKRRKAGASAGASQGQWEDDYELVPCE--G	547							
Db	293	IIMVLKQTNWNFMELGYPLIQNWWTR--RKVRQEHGPERKISFPQWEKDYNLQPMNAYG	349							
Qy	548	LFDEYLEMVLQFGVTFIVAAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIG	607							
Db	350	LFDEYLEMILQFGFTTIFVAAFPALPLALLNNIIEIRLDAYKFVQTQWRRPLASRAKDIG	409							
Qy	608	IWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRW-----TRAHDLRGFLNFTLA	657							
Db	410	IWYGILEGIGILSVITNAFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGVYNASLS	469							
Qy	658	-----RAPSSFAAAHNRTCRYRAFRDDDGH-----YSQTYWNLLAIRLAFV	698							
Db	470	VFRISDFENRSEPESDGSEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFHWVLAARLAFI	529							
Qy	699	IVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGS	758							
Db	530	IVFEHLVFCIKHLISYLPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNKG	589							
Qy	759	ELSSHW 764								
Db	590	AHHNEW 595								

RESULT 3

US-10-104-047-3116

; Sequence 3116, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

Query Match 22.1%; Score 912.5; DB 2; Length 475;
Best Local Similarity 38.0%; Pred. No. 7.2e-88;
Matches 202; Conservative 89; Mismatches 143; Indels 97; Gaps 12;

Qy	274	MALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFP	333
		: : : : : : :	
Db	1	MAVWATVFLFQWKRRAVIAYDWDLIDWEEEE-----	32
Qy	334	ERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNGTLLA-AWA-----SR	387
		: : : : : : : : :	
Db	33	-----ICVVIAAVFGIVIRVTV-----STFAAFKVALIRNNSQ	67
Qy	388	IASLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDATLKVFIFQFVNFYS	445
		: : : : : : : : : : : : : : : :	
Db	68	VAT-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPTSESEWENSFTLKMFLQFVNLNS	126
Qy	446	SPVYIAFFKGRFVGYPGNYHTLFG--VRNEECAAGGLIELAQELLVIMVGKQVINNMQEV	504
		: : : : :	
Db	127	STFYIAFFLGRFTGHGPAYLRLINRWRLEECHPSGCLIDLQCMQGIIMVLKQTNWNFMEL	186
Qy	505	LIPKLKGWQKFLRLSKRRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFV	562
		: : : : :	
Db	187	GYPLIQNWWRTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFT	243
Qy	563	TIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVI	622
Db	244	TIFVAAPLAPLALLLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWIYGILEGIGILSVI	303
Qy	623	SNAFLLAFSSDFLPRAYYRW-----TRAHDLRGLFNFTLA-----R	658
		: : : : : : : : : :	
Db	304	TNAFVIAITSDFIPRLVYAYKYGPCAQGEAGQKCMVGVNASLSVFRISDFENRSEPE	363
Qy	659	APSSFAAAHNRTCRYAFRDRDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLD	713
		: : : : : : : :	
Db	364	DGSEFSGTPLKYCRYRDRDPHSLVPYGYTLQFVHVLAARLAFIIVFEHLVFCIKHLIS	423
Qy	714	LLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW	764
		: : : : : : : : : : : : : : :	
Db	424	YLIPDLPKDLDRMRREKYLIOEMMYEALERLOKERKRRKNGKAHHNEW	474

RESULT 4

US-10-108-260A-4483

; Sequence 4483, Application US/10108260A

; Patent No. 7193069

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 7193069e1 full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4483

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-108-260A-4483

Query Match 21.2%; Score 873.5; DB 3; Length 642;
 Best Local Similarity 39.2%; Pred. No. 1.7e-83;
 Matches 192; Conservative 93; Mismatches 172; Indels 33; Gaps 11;

```

Qy      5 QDGNTTVH---YALLSASWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPNVLL 61
      :| :| :| : : | | || | | :|| :| :: : | : || | :||
Db      116 RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLMPTKMYH--INETRGLLK--KINSVLQ 171

Qy      62 EVVPDVPEYYSCR-----FRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 111
      :: :| : | | | | | | | | :|| | | | :||| :|
Db      172 KITDPIQPKVAEHRPQTMKRLSYPPFSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT 230

Qy      112 YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPEGPQAPRLNQRQVLQFQHWARWGKWN 171
      | : :| || | | :|| :||| : : : | :| :| :|| :| :
Db      231 CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEAWARYGVFY 284

Qy      172 KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSIDIPTQELCGS 231
      ||||| | :||| :| :||| | | | :||| :| :||| :| :| :| :|
Db      285 KYQPIDLVKRYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ 344

Qy      232 KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA 290
      : : |||| | : : ||||| | :| :||| :| :| :||| :| :|||
Db      345 RHNITMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM 404

Qy      291 TLAYRWDSCSDYEDTEERPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGS 345
      | ||| : :| :| :| :| :| | : : | | | : | | |
Db      405 RLNYRWDLTGFEEDHDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNL 462

Qy      346 VVIVVMVAVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFIILS 405
      | | :| :| : : :| :| :| : : : : : : : | :||| | :|
Db      463 VSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVILLD 522

Qy      406 KIYVSLAHLVLRWEMHRTQTKFEDAFTLKVFIFQVFNFYSSPVYIAFFKGRFVGYPGNYH 465

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US-09-270-767-45552

Query Match 19.3%; Score 796; DB 2; Length 425;
Best Local Similarity 41.1%; Pred. No. 1.7e-75;
Matches 171; Conservative 85; Mismatches 128; Indels 32; Gaps 9;

http://es.ScoreAccessWeb/GetItem.action?AppId=105525...10-552-515-1_copy_157_933.ra1&ItemType=4&startByte=0 (8 of 18)10/10/2008 8:52:47 AM

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Db      294  APFFALLNNILEMRDLAKLLTHHKRPVSQRVRDIGVWYRILDCIGKLSVITNGFIIAFT 353
      || ||||| :|:||||| : :|||:| :|||:| :| :|:|:| |:|:|
Qy      632  SDFLPR-AYYRWTRAHDLRGFLNFTLAR-----APSSFAAAHN----RTCRYRAFR 677
      || :|| : : | |:||||: :|: :| : |||| ||
Db      354  SDMPRLVRHXVKNQGTLDGYLNFTLSEFKVIDSPITYSLAGDLSNITTCRYTDFR 409

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RESULT 6

```

US-10-108-260A-3990
; Sequence 3990, Application US/10108260A
; Patent No. 7193069
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 7193069el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3990
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3990

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Query Match      16.6%; Score 684.5; DB 3; Length 483;
Best Local Similarity 35.1%; Pred. No. 1.7e-63;
Matches 171; Conservative 95; Mismatches 168; Indels 53; Gaps 14;

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Qy      323  PITGEDE-----PYFFERSRARRMLAGSVVIVVMVAVVMCLV----SIILYRAIM 369
      | :| | | | | | | | :| :| :| :| :| :| :| :| :| :| :|
Db      2   PAVSEEEEMALQLINCPDYKLRPYQHSYLRSTVILV--LTLLMICLMIGMAHVLVVYRVLA 59

Qy      370  AIVVSRSGNTLLAAWASRIASLTGSVVNLVFLILILSKIYVSLAHVLTWRWEMHRTQTKFED 429
      : : | | | : :| :| :| :| :| :| :| :| :| :| :| :|
Db      60  SALFSSSAVPFLEEQVTTAVVVTGALVHYVTIVIMTKINRRVALKLCDFEMPRTFSERES 119

Qy      430  AFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLFGV--RNEECAAGGCLIELAQEL 488
      ||:| | | :|| :||| || :|| | :| :| | | :| :| :|
Db      120  RFTIRFFTLQFFTHFSSLIYIAFILGRINGHPGKSTRLAGLWKLECHASGCMMDLFVQM 179

Qy      489  LVIMVGKQVINNMQEVLIPLKLGWWQKFLRLSKKRKAGASAGASQGP---WEDDYELVP 544
      :|| || :| | | | :| | :| | :| | :| | | :| | |
Db      180  AIIMGLKQTLNSNCVEYLVF-----WVTHKCRS--LRAESGHLPRDPELRDWRNRYLNP 232

Qy      545  CE--GLFDEYLEMVLQFGVFTIFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAER 602
      |||:|:|:|:|:| | || | | | | | | | | | | | | | :
Db      233  VNTFSLFDEFMEMMIQYGFTTIFVAAPPLAPLLALFSNLVEIRLDAIKMVWLQRRLVPRK 292

Qy      603  AQDIGIFWHILAGLTHLAVISNAFLAFSSDFLPRAYYRW-----TRAHDLRGFL 652
      |:| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      293  AKDIGTWLQVLETIGVLAVIANGMVIAFTSEFIPRVVYKYRSPCLKEGNSTVDCLKGYV 352

```

```

Qy      653 NFTLA-----RAPSSFAAAHNRT-CRYRAFRD-DDGHYSQTYWLLLAIRLAFVIVFEH 703
      | :|:      : |      : | | ||| :|: | ::|: :| ||||| |||: ||
Db      353 NHSLSVFHTKDFQDPDGIEGSENVTLCRYRDYRNPPDYNFSEQFWFLLAIRLAFVILFEH 412

Qy      704 VVFSVGRLLDLLVPDIPESVEIKV-KREYLLAKQALAENEVLFGTNGTKDEQPKGSELSS 762
      | : :      |||||: || : | : : | : : | | | : :
Db      413 VALCIKILIAAWFVPDIPQSVKNKVLEVQYQRLREKMMWHGRQRLGGVGAGSRPP-----MPA 468

Qy      763 HWTPTFTV 769
      | || ::
Db      469 HPTPASI 475
  
```

RESULT 7

```

US-10-108-260A-3644
; Sequence 3644, Application US/10108260A
; Patent No. 7193069
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 7193069el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3644
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3644
  
```

```

Query Match      14.4%; Score 594.5; DB 3; Length 660;
Best Local Similarity 24.1%; Pred. No. 1.1e-53;
Matches 171; Conservative 122; Mismatches 231; Indels 185; Gaps 20;
  
```

```

Qy      72 YSCRFRVNKLPRFLG-SDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLG----- 121
      : | | | | | | | | | | | | | | | | | | | |
Db      100 FTYRTRQN----FKGFDNDNDDFLTMAECQFII-----KHELENLRAKDEKMIPGY 146

Qy      122 -----IHQLLAEGVLSAAFLHDGPFKTPPEGPQAPRLNQOVLFQHW-ARWGK 169
      : | | : | | | | | | | | | | | | | | | |
Db      147 PQAKLYPGKSLRLRLTSGIVIQVFPLHDS-----EALKKLEDTWYTRFAL 192

Qy      170 WNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTGLVFLVGCFLVFSDIPTQELC 229
      |||||: | | |||| : |||| : | : | | : | ||: |
Db      193 --KYQPIDSIRGYFGETIALYFGFLEYFTFALIPMAVIG----- 229

Qy      230 GSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS 289
      | : | | | : | | | : | : | : | : | | |
Db      230 -----LPYYLFVWE-----DYDKYVIFASFNLWSTVILELWKRGC 265

Qy      290 ATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIV 349
  
```

```

      | : ||| : | || | : | |||::| : | : | : |
Db      266 ANMTYRWGTLMKRKFEEPRPGFHG---VLGINSITGKEEPLYPYKQRLRIYLVSLPFV 322

Qy      350 VMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVVNLVFIILSKIYV 409
      : : : | : | : : : | | : | : : | | : : |
Db      323 CLCLYFSLYVMMIYFDMEVWALGLHENSNG---SEWTS-VLLYVPSIIYAIIVIEIMNRLYR 378

Qy      410 SLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGPNGNYHTLFG 469
      | || || || : : : || | : | : | : | |||
Db      379 YAAEFLTSWENHRLESAYQNHILKVLVFNFLNCFASLFYIAFV----- 422

Qy      470 VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGKWW--QKFLRSKKRKAGA 527
      : : : | | | : : | : | : | : | : | : | : |
Db      423 LKDMKL-----LRQSLATLLITSQILNQIMESFLP----YWLQRKHGVRVRKRVQAL 470

Qy      528 SAGASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLALLNNWVEI 584
      | : | : | : | | : | : | : | : | : | : |
Db      471 KADIDATLYEQVILEKEMGTLYLGTDDYLELFLQFGYVSLFSCVYPLAAFAVLNNFTEV 530

Qy      585 RLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRWTR 644
      || | : || : | : | : | : : : : | : | : : :
Db      531 NSDALKMCRCVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSPQV--NAVFPESK 588

Qy      645 AHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHSQTYWNLLAIRLAFVIVFEHV 704
      | || : : : : : : : : : : : : : : : |
Db      589 A-DL-----ILIVVAVEHA 601

Qy      705 VFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGINGTKDE 753
      : : : : | : || | : : | : : : | : : : | : |
Db      602 LLALKFILAFAIPDKPRHIQMKLARLEFESLEALKQQQMKLVITENLKEE 650

```

RESULT 8

US-09-876-997-457

; Sequence 457, Application US/09876997

; Patent No. 7060479

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Jobert, Severin

; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

; FILE REFERENCE: 78.US4.CIP

; CURRENT APPLICATION NUMBER: US/09/876,997

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 09/731,872

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/187,470

; PRIOR FILING DATE: 2000-03-06

; PRIOR APPLICATION NUMBER: US 60/169,629

; PRIOR FILING DATE: 1999-12-08

; NUMBER OF SEQ ID NOS: 482

; SOFTWARE: Patent.pm

; SEQ ID NO 457

; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-997-457

Query Match 10.0%; Score 411.5; DB 3; Length 393;
Best Local Similarity 23.8%; Pred. No. 1.7e-34;
Matches 111; Conservative 95; Mismatches 172; Indels 89; Gaps 11;

Qy 292 LAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRRARRMLAGSVVIVVM 351
: ||| : | ||| | : | |||: || : | | : | :
Db 1 MTYRWGTLLMKRKFEPRPGFHG---VLGINSITGKEEPLYPYKRLRIYLVSLPFVCL 57

Qy 352 VAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNVLFILILSKIYVSL 411
: :: | : | : : : | | : | : | : | :
Db 58 CLYFSLYVMMIYFDMEVWALGLHENS---SEWTS-VLLVVPSTIIYAIVIEIMNRLYRYA 113

Qy 412 AHVLTREWEMHRTQTKFEDAFTLVKFIFQFVNYSPPVYIAFFKGRFVGYPGNYHTLFGVR 471
| || || || :: :: ||| : | | : | ||| : :
Db 114 AEFLTSWENHRLSEAYQNHLLKVLVFNFLNCFASLFYIAFV-----LK 157

Qy 472 NEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKKGW---QKFLRLSKKRKAGASA 529
: : | | | :: | : | : | : | : | : | :
Db 158 DMKL-----LRQSLATLLITSQILNQIMESFLP---YWLQRKHGVRVKKRVQALKA 205

Qy 530 GASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLAFALLNNWVEIRL 586
: | : | | ||: ||| : ||| : || | | : ||| : | :
Db 206 DIDATLYEQVILEKEMGYTLGTFDDYLELFLQFGYVSLFSCVYPLAAFAVLNNFTVEVNS 265

Qy 587 DARKFVCEYRRPVAERAQDIGHWIFHLAGLTHLAVISNAFLLAFSSDFLPRAYRWTRAH 646
| | : || : | : ||: | : : ||: | | : | : : ||
Db 266 DALMKCRVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSPOV--NAVFPESKA- 322

Qy 647 DLRGFLNFTLARAPSSFAAAHNRTCRYAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVF 706
| | : | : | : | : | : | : | : | : | :
Db 323 DL-----ILIVVAVEHALL 336

Qy 707 SVGRLLDLLVPDIPESVEIKVKREYLLAKQALAENEVLFGTNGTKDE 753
: : | : | : ||: | : : ||: | : : | : | :
Db 337 ALKFI LAFAPDKPRHIQMKLARLEFESLEALKQQQMKLV TENLKEE 383

RESULT 9

US-10-643-836-457

; Sequence 457, Application US/10643836

; Patent No. 7271243

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Jobert, Severin

; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

; FILE REFERENCE: 78.US3.REG

; CURRENT APPLICATION NUMBER: US/10/643,836

```

; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 457
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-643-836-457

```

Query Match 10.0%; Score 411.5; DB 3; Length 393;
 Best Local Similarity 23.8%; Pred. No. 1.7e-34;
 Matches 111; Conservative 95; Mismatches 172; Indels 89; Gaps 11;

```

Qy      292 LAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVM 351
      : ||| : ||| : | ||| : | ||| : | | : | : | :
Db      1 MTYRWGTLLMKRKFEEPRPGFHG---VLGINSITGKEPLYPSYKRLRIYLVSLPFVCL 57

Qy      352 VAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSL 411
      : :: | : | : : : | | : | : | : | : | : | :
Db      58 CLYFSLYVMMIYFDMEVWALGLHENS---SEWTS-VLLYVPSIIYAIVIEIMNRLRYA 113

Qy      412 AHVLTWRWEMHRTQTKEFAFTLKVFIQFVNFISSPVYIAFFKGRFVGYPGNYHTLFGVR 471
      | || || || : : : : ||| : | : | : | ||| : :
Db      114 AEFLTSWENHRLESAYQNHLILKVLVFNFLNCFASLFYIAFV-----LK 157

Qy      472 NEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKKGW---QKFLRLSKKRKAGASA 529
      : : | | | : : | : | : | : | : | : | : |
Db      158 DMKL-----LRQSLATLLITSQILNQIMESFLP----YWLQRKHGVRVKRVQALKA 205

Qy      530 GASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAA CPLAPL FALLNNWVEIRL 586
      : | : | : | ||| : | : | : | : | : | : | :
Db      206 DIDATLYEQVILEKEMGYTLGTFDDYLEFLQFGYVSFLSCVYPLAAFAVLNNFTVEVNS 265

Qy      587 DARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRWTRAH 646
      || | : || : | : : || : : : || : | : | : |
Db      266 DALMKCRVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSQV--NAVFPESKA- 322

Qy      647 DLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHSYQTYWNLLAIRLAFVIVFEHVVF 706
      || : : : : : : : : : : : : : : : :
Db      323 DL-----ILIVVAVEHALL 336

Qy      707 SVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDE 753
      : : : | : | : : : | : : : : | : | : |
Db      337 ALKFILAFaipdkprhiQMKLARLEFESLEALKQQQMKLV TENLKEE 383

```

RESULT 10

; ORGANISM: Drosophila melanogaster
US-09-270-767-32253

Query Match 8.0%; Score 329.5; DB 2; Length 366;
Best Local Similarity 33.8%; Pred. No. 8.7e-26;
Matches 78; Conservative 48; Mismatches 86; Indels 19; Gaps 5;

```
Qy      11 VHYALLSASWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPNVL-----LEV 64
      : : : | || ||| |:|::|::|:| : : : : :| : : |
Db      139 IWFVKIHAPLEVLRRYAEILKLRMPMKEIPGMSVVNRSTKSVFSSLKHVFQFFLRNIYVD 198

Qy      65 PDVPPEYYSCRFRV--NKLPRFLGSDNQDTFFTSTKRHQILFEIL--AKTPYGHEKKNLL 120
      :: |: : || :: :| || |||: |:|: || : | ::
Db      199 EEIPFK-RAHRTAIYSRDKEYLFDIRQDCFFTTAVSRIVEFILDRQRFPAKNQHDMAF 257

Qy      121 GIHQLLAEGVLSAAFPPLHDGPFKTPPEGQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
      || |:|:| |||:| ||| | :|::| || |:| ||| ::
Db      258 GIERLIAEGVYSAAAYPLHDGEITETG-----TMRALLYKHWASVPKWYRYQPLDDIK 309

Qy      181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
      ||| |: | ||| |||:| || |:|:| || |:|:| ||| ::
Db      310 EYFGVKIGLYFAWLGYTYMLLLASIVGVICFLYSWFSKKNYVPVKDICQS 360
```

RESULT 12

US-09-270-767-47470

; Sequence 47470, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 47470

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-47470

Query Match 8.0%; Score 329.5; DB 2; Length 366;
Best Local Similarity 33.8%; Pred. No. 8.7e-26;
Matches 78; Conservative 48; Mismatches 86; Indels 19; Gaps 5;

```
Qy      11 VHYALLSASWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPNVL-----LEV 64
      : : : | || ||| |:|::|::|:| : : : : :| : : |
Db      139 IWFVKIHAPLEVLRRYAEILKLRMPMKEIPGMSVVNRSTKSVFSSLKHVFQFFLRNIYVD 198

Qy      65 PDVPPEYYSCRFRV--NKLPRFLGSDNQDTFFTSTKRHQILFEIL--AKTPYGHEKKNLL 120
      :: |: : || :: :| || |||: |:|: || : | ::
Db      199 EEIPFK-RAHRTAIYSRDKEYLFDIRQDCFFTTAVSRIVEFILDRQRFPAKNQHDMAF 257
```

http://es.ScoreAccessWeb/GetItem.action?AppId=10552...0-552-515-1_copy_157_933.rai&ItemType=4&startByte=0 (16 of 18)10/10/2008 8:52:47 AM

; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 47033
 ; LENGTH: 189
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-47033

Query Match 7.0%; Score 290; DB 2; Length 189;
 Best Local Similarity 37.8%; Pred. No. 5.1e-22;
 Matches 62; Conservative 25; Mismatches 59; Indels 18; Gaps 4;

Qy 93 FFTSTKRHQILFEILAKTPY--GHEKKNLLGIIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQ 150
 | :: |: |: || : : || : ||| :: |: || : |: |||
 Db 39 FLDASTRYSIINFILQQRQFVEGEETADNLGIEKLVQDGVYTCAYTLHD----- 87
 Qy 151 APRLNQRQVLFQHWARWGKWNKYQLDHHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTL 210
 : | | : || || |||| : || ||||| ||||| ||| : | : | |
 Db 88 ---KDDRDRLLKEWANISKWKNLQPLDQIKDYFGAKVALYFAWLGFYTGMLIPISVFGVL 144
 Qy 211 VFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSAC 253
 || | || : ::| : || | | : | : |
 Db 145 CFLYGFITWNSDPISRDICDDNGTI-MCPQCDCRSCDYWRNLNETC 187

RESULT 15

US-09-270-767-31722
 ; Sequence 31722, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 31722
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-31722

Query Match 6.2%; Score 255.5; DB 2; Length 199;
 Best Local Similarity 29.8%; Pred. No. 2.7e-18;
 Matches 59; Conservative 46; Mismatches 64; Indels 29; Gaps 5;

Qy 261 LFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTA 320
 | |: || |: ||: |||: ||: ||| || | :| : : | |||: | |
 Db 11 LIDNNMTVVFAFSMAIWAUVVYLEFWKRYAGLVHRWGLTGFTHHVHRPQYLARISRT- 69

Qy	321	PNPITGEDEPYFPPERSRARRMLAGSV-----VIVVMVAVVVMCLVSIILY	365
		: : :: : : : : : :	
Db	70	-KKLAG--KAYEQDQTKGRTILDPDVPFWSFKFLPNFTSYSIMVLFICISVIAIAGIIY	126
Qy	366	RAIMAIVVSRSGNTLLAAWAS-----RIASLTGSVVNLVFILILSKIYVSLAHVLRWEM	420
		: : :: : : : : : :	
Db	127	R-----MAQRASHSILGSENSMTFKVMILPMTAGIIDLIVISLDMVYSNLAVKLTNYEY	181
Qy	421	HRTQTKFEDAFTLKVFIF	438
		::: : :	
Db	182	CRTQTEYDESLTIKNYVF	199

Search completed: June 24, 2008, 15:27:19
 Job time : 281 secs

SCORE: 0